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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/890,646

DATE: 01/03/2002  
TIME: 21:57:13

Input Set: I890646.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: AYABE, SHINICHI  
2 AOKI, TOSHIO  
3 AKASHI, TOMOYOSHI  
4 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE SYNTHASE  
5 <130> FILE REFERENCE: JKM-001  
6 <140> CURRENT APPLICATION NUMBER: US/09/890,646  
7 <141> CURRENT FILING DATE: 2001-08-02  
8 <150> EARLIER APPLICATION NUMBER: PCT/JP00/00596  
9 <151> EARLIER FILING DATE: 2000-02-04  
10 <160> NUMBER OF SEQ ID NOS: 14  
11 <170> SOFTWARE: PatentIn Ver. 2.1  
12 <210> SEQ ID NO 1  
13 <211> LENGTH: 1895  
14 <212> TYPE: DNA  
15 <213> ORGANISM: Glycyrrhiza echinata  
16 <220> FEATURE:  
17 <221> NAME/KEY: CDS  
18 <222> LOCATION: (144)..(1712)  
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21 acttcctcct atactcgact ctttggttatt agttatcatt attattatta caccattaaa 120  
22 gtagcaaaga tcaaacaaac acc atg ttg gtg gaa ctt gca att act ctg ttg 173  
23 Met Leu Val Glu Leu Ala Ile Thr Leu Leu  
24 1 5 10  
25 gtg ata gcc ctg ttc ata cac ctg cgt ccc aca cta agt gca aaa tca 221  
26 Val Ile Ala Leu Phe Ile His Leu Arg Pro Thr Leu Ser Ala Lys Ser  
27 15 20 25  
28 aag tcc ctt cgc cac ctc cca aac cct cca agt cca aaa ccc cgt ctc 269  
29 Lys Ser Leu Arg His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu  
30 30 35 40  
31 cca ttt gtg ggt cac ctt cac ctt tta gac aaa ccc ctt ctc cac tac 317  
32 Pro Phe Val Gly His Leu His Leu Leu Asp Lys Pro Leu Leu His Tyr  
33 45 50 55  
34 tcc ctc atc gac cta agc aaa cgc tat ggt ccg ctt tac tcc ctc tac 365  
35 Ser Leu Ile Asp Leu Ser Lys Arg Tyr Gly Pro Leu Tyr Ser Leu Tyr  
36 60 65 70  
37 ttc ggt tcc atg cca acc gtt gta gcc tcc acc cct gaa ctt ttc aaa 413  
38 Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys  
39 75 80 85 90  
40 ctc ttc ctc caa act cac gag gcc tct tcc ttc aac aca agg ttc caa 461  
41 Leu Phe Leu Gln Thr His Glu Ala Ser Ser Phe Asn Thr Arg Phe Gln  
42 95 100 105  
43 acc tct gcc att agg cgc cta acc tac gac aac tct gtt gcc atg gtt 509  
44 Thr Ser Ala Ile Arg Arg Leu Thr Tyr Asp Asn Ser Val Ala Met Val

45					110					115					120					
46	ccc	ttt	ggt	cct	tac	tgg	aag	ttc	att	agg	aag	ctc	atc	atg	aac	gac				557
47	Pro	Phe	Gly	Pro	Tyr	Trp	Lys	Phe	Ile	Arg	Lys	Leu	Ile	Met	Asn	Asp				
48				125					130					135						
49	ctc	ctc	aat	gcc	aca	act	gtg	aac	aag	ttg	agg	cct	tta	agg	agc	caa				605
50	Leu	Leu	Asn	Ala	Thr	Thr	Val	Asn	Lys	Leu	Arg	Pro	Leu	Arg	Ser	Gln				
51			140					145						150						
52	gaa	atc	cga	aag	gtc	ctc	agg	gtg	atg	gca	cag	agt	gct	gag	tct	cag				653
53	Glu	Ile	Arg	Lys	Val	Leu	Arg	Val	Met	Ala	Gln	Ser	Ala	Glu	Ser	Gln				
54	155						160					165				170				
55	gtc	cca	ctt	aat	gtc	acc	gag	gag	ctt	ctc	aag	tgg	acc	aac	agc	acc				701
56	Val	Pro	Leu	Asn	Val	Thr	Glu	Glu	Leu	Leu	Lys	Trp	Thr	Asn	Ser	Thr				
57					175					180					185					
58	atc	tcg	agg	atg	atg	ctt	ggg	gaa	gca	gag	gaa	atc	agg	gac	ata	gca				749
59	Ile	Ser	Arg	Met	Met	Leu	Gly	Glu	Ala	Glu	Glu	Ile	Arg	Asp	Ile	Ala				
60				190					195					200						
61	cgt	gac	gtg	ctt	aag	atc	ttt	ggg	gag	tat	agt	ctc	acc	gac	ttc	atc				797
62	Arg	Asp	Val	Leu	Lys	Ile	Phe	Gly	Glu	Tyr	Ser	Leu	Thr	Asp	Phe	Ile				
63			205					210						215						
64	tgg	ccc	ttg	aag	aaa	ctc	aag	gtt	ggg	caa	tac	gag	aag	agg	att	gac				845
65	Trp	Pro	Leu	Lys	Lys	Leu	Lys	Val	Gly	Gln	Tyr	Glu	Lys	Arg	Ile	Asp				
66		220					225						230							
67	gat	ata	ttc	aac	agg	ttt	gac	ccc	gtc	att	gag	agg	gtc	atc	aag	aaa				893
68	Asp	Ile	Phe	Asn	Arg	Phe	Asp	Pro	Val	Ile	Glu	Arg	Val	Ile	Lys	Lys				
69	235					240					245					250				
70	aga	cag	gag	att	agg	aag	aag	agg	aag	gag	agg	aat	ggt	gag	atc	gag				941
71	Arg	Gln	Glu	Ile	Arg	Lys	Lys	Arg	Lys	Glu	Arg	Asn	Gly	Glu	Ile	Glu				
72				255					260						265					
73	gag	ggt	gaa	cag	agt	gtg	gtt	ttt	ctc	gac	act	ttg	ctc	gat	ttt	gct				989
74	Glu	Gly	Glu	Gln	Ser	Val	Val	Phe	Leu	Asp	Thr	Leu	Leu	Asp	Phe	Ala				
75			270					275						280						
76	gag	gac	gag	acc	atg	gag	atc	aaa	atc	acc	aag	gaa	caa	atc	aag	ggc				1037
77	Glu	Asp	Glu	Thr	Met	Glu	Ile	Lys	Ile	Thr	Lys	Glu	Gln	Ile	Lys	Gly				
78			285					290												

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95      Val Gln Glu Cys Glu Val Asp Gly Tyr Val Ile Pro Glu Gly Ala Leu
96      380                               385                               390
97      atc ctt ttc aat gtt tgg gcc gtc gga aga gac cca aaa tac tgg gac      1373
98      Ile Leu Phe Asn Val Trp Ala Val Gly Arg Asp Pro Lys Tyr Trp Asp
99      395                               400                               405                               410
100     agg ccc act gag ttc cgt ccc gaa agg ttc tta gaa aat gtg ggt gaa      1421
101     Arg Pro Thr Glu Phe Arg Pro Glu Arg Phe Leu Glu Asn Val Gly Glu
102                               415                               420                               425
103     ggg gat caa gcc gtt gac ctt agg ggt caa cat ttc caa ctt ctt ccg      1469
104     Gly Asp Gln Ala Val Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro
105                               430                               435                               440
106     ttt ggg tct gga agg agg atg tgc cct ggc gtc aat ttg gcc act gcg      1517
107     Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ala
108                               445                               450                               455
109     gga atg gcc aca ctg ctt gcg tca gtt atc cag tgc ttt gat ctc agc      1565
110     Gly Met Ala Thr Leu Leu Ala Ser Val Ile Gln Cys Phe Asp Leu Ser
111     460                               465                               470
112     gta gtg ggc cca cag gga aag ata ttg aag ggc aat gat gcc aag gtt      1613
113     Val Val Gly Pro Gln Gly Lys Ile Leu Lys Gly Asn Asp Ala Lys Val
114     475                               480                               485                               490
115     agc atg gaa gag aga gct gga ctc acg gtt cca agg gca cat aac ctc      1661
116     Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala His Asn Leu
117                               495                               500                               505
118     atc tgt gtc ccg gtt gca aga tca agt gcc gta ccc aaa ctc ttt tcg      1709
119     Ile Cys Val Pro Val Ala Arg Ser Ser Ala Val Pro Lys Leu Phe Ser
120                               510                               515                               520
121     tcg taaaacatac gcgcgacacc agaaagctgc catggcatga tgctttttat      1762
122     Ser
W--> 123
124     ataataattt tcaataaggt atcaatcaat gatatataga caatgatacc catatatcat      1822
125     ctctgcgact agtctctctt tggtagagta tgttgtaaca gcttaaactt atataatttt      1882
126     tactgcgata tcc      1895
127     <210> SEQ ID NO 2
128     <211> LENGTH: 523
129     <212> TYPE: PRT
130     <213> ORGANISM: Glycyrrhiza echinata
131     <400> SEQUENCE: 2
132     Met Leu Val Glu Leu Ala Ile Thr Leu Leu Val Ile Ala Leu Phe Ile
133     1 5 10 15
134     His Leu Arg Pro Thr Leu Ser Ala Lys Ser Lys Ser Leu Arg His Leu
135     20 25 30
136     Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Val Gly His Leu
137     35 40 45
138     His Leu Leu Asp Lys Pro Leu Leu His Tyr Ser Leu Ile Asp Leu Ser
139     50 55 60
140     Lys Arg Tyr Gly Pro Leu Tyr Ser Leu Tyr Phe Gly Ser Met Pro Thr
141     65 70 75 80
142     Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
143     85 90 95
144     Glu Ala Ser Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg

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196      Arg Ser Ser Ala Val Pro Lys Leu Phe Ser Ser
197          515          520
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199 <211> LENGTH: 422
200 <212> TYPE: DNA
201 <213> ORGANISM: Glycyrrhiza echinata
202 <400> SEQUENCE: 3
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204      ccagtgccttt gatctcagcg tagtgggccc acagggaaaag atattgaagg gcaatgatgc 120
205      caaggttagc atggaagaga gagctggact cacggttcca agggcacata acctcatctg 180
206      tgtcccgggtt gcaagatcaa gtgccgtacc caaactcttt tcgtcgtaaa acatacgcgc 240
207      gacaccacag aaagttgccca tggcatgatg ctttttatat aataattttc aataagggtat 300
208      caatcaatga tatatagaca atgataccca tatatcatct tcacgactag tctctctttg 360
209      gtacagtatg ttgtaacagc ttaaattctat ataattttta ctgcgatatc catttcctga 420
210      tt 422
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212 <211> LENGTH: 28
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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220 <211> LENGTH: 29
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
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233 <400> SEQUENCE: 6
234      Leu Pro Phe Gly Ser Gly Arg Arg Ser Cys
235          1          5          10
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237 <211> LENGTH: 12
238 <212> TYPE: PRT
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
242 <400> SEQUENCE: 7
243      Tyr Leu Gln Ala Ile Val Lys Glu Thr Leu Arg Leu
244          1          5          10

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Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

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VERIFICATION SUMMARY  
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Line ? Error/Warning

Original Text

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123 W Invalid/Missing Amino Acid Numbering

272 W "N" or "Xaa" used: Feature required

htnscnttyr gnnnnggnms nmg